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## SEQUENCE LISTING

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 HINUMA, Shuji  
 HASHIMOTO, Tadatoshi  
 TANAKA, Yasuhiro

<120> Novel Screening Method

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<150> PCT/JP2004/005947

<151> 2004-04-23

<150> JP 2003-122464

<151> 2003-04-25

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<211> 453

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<213> Human

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Leu	Ile	Leu	Val	Tyr	Leu	Ile	Ile	Phe	Val	Met	Gly	Leu	Leu	Gly	Asn
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Gln	Lys	Glu	Val	Thr	Asp	His	Met	Val	Ser	Leu	Ala	Cys	Ser	Asp	Ile
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Leu	Val	Phe	Leu	Ile	Gly	Met	Pro	Met	Glu	Phe	Tyr	Ser	Ile	Ile	Trp
			85						90					95	
Asn	Pro	Leu	Thr	Thr	Ser	Ser	Tyr	Thr	Leu	Ser	Cys	Lys	Leu	His	Thr
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Val	Thr	Ser	Ala	Leu	Val	Ala	Leu	Pro	Leu	Leu	Phe	Ala	Met	Gly	Thr
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Glu	Tyr	Pro	Leu	Val	Asn	Val	Pro	Ser	His	Arg	Gly	Leu	Thr	Cys	Asn
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Arg	Ser	Ser	Thr	Arg	His	His	Glu	Gln	Pro	Glu	Thr	Ser	Asn	Met	Ser
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Ile	Cys	Thr	Asn	Leu	Ser	Ser	Arg	Trp	Thr	Val	Phe	Gln	Ser	Ser	Ile

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Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser				240
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Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu				
	260		265	270
Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile				
	275		280	285
Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile				
	290		295	300
Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg				
305		310		315
Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser				320
	325		330	335
Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg				
	340		345	350
Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala				
	355		360	365
Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser				
	370		375	380
Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser				
385		390		395
Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu				400
	405		410	415
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tgccgcctgt	cgctgcagca	cgccaaccac	gagaagcgcc	tgccgcgtaca	tgccgcactcc	1140

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<211> 456
<212> PRT
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              20              25              30
Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Val Gly Ile Leu Gly Asn
              35              40              45
Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
              50              55              60
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
              65              70              75              80
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
              85              90              95

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Asn	Pro	Leu	Thr	Thr	Pro	Ser	Tyr	Ala	Leu	Ser	Cys	Lys	Leu	His	Thr
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		115					120					125			
Leu	Ser	Phe	Glu	Arg	Tyr	Ile	Ala	Ile	Cys	His	Pro	Phe	Lys	Tyr	Lys
	130					135					140				
Ala	Val	Ser	Gly	Pro	Arg	Gln	Val	Lys	Leu	Leu	Ile	Gly	Phe	Val	Trp
145					150					155					160
Val	Thr	Ser	Ala	Leu	Val	Ala	Leu	Pro	Leu	Leu	Phe	Ala	Met	Gly	Ile
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Glu	Tyr	Pro	Leu	Val	Asn	Val	Pro	Thr	His	Lys	Gly	Leu	Asn	Cys	Asn
		180						185					190		
Leu	Ser	Arg	Thr	Arg	His	His	Asp	Glu	Pro	Gly	Asn	Ser	Asn	Met	Ser
		195					200				205				
Ile	Cys	Thr	Asn	Leu	Ser	Asn	Arg	Trp	Glu	Val	Phe	Gln	Ser	Ser	Ile
	210					215					220				
Phe	Gly	Ala	Phe	Ala	Val	Tyr	Leu	Val	Val	Leu	Ala	Ser	Val	Ala	Phe
225					230					235					240
Met	Cys	Trp	Asn	Met	Met	Lys	Val	Leu	Met	Lys	Ser	Lys	Gln	Gly	Thr
			245						250					255	
Leu	Ala	Gly	Thr	Gly	Pro	Gln	Leu	Gln	Leu	Arg	Lys	Ser	Glu	Ser	Glu
		260						265					270		
Glu	Ser	Arg	Thr	Ala	Arg	Arg	Gln	Thr	Ile	Ile	Phe	Leu	Arg	Leu	Ile
		275					280					285			
Val	Val	Thr	Leu	Ala	Val	Cys	Trp	Met	Pro	Asn	Gln	Ile	Arg	Arg	Ile
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Met	Ala	Ala	Ala	Lys	Pro	Lys	His	Asp	Trp	Thr	Arg	Thr	Tyr	Phe	Arg
305					310					315					320
Ala	Tyr	Met	Ile	Leu	Leu	Pro	Phe	Ser	Asp	Thr	Phe	Phe	Tyr	Leu	Ser
			325						330					335	
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			340					345					350		
Lys	Val	Phe	Trp	Gln	Val	Leu	Cys	Cys	Arg	Leu	Thr	Leu	Gln	His	Ala
		355					360					365			
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	370					375					380				
Thr	Ser	Ser	Ala	Arg	Ser	Pro	Leu	Ile	Phe	Leu	Ala	Ser	Arg	Arg	Ser
385					390					395					400
Asn	Ser	Ser	Ser	Arg	Arg	Thr	Asn	Lys	Val	Phe	Leu	Ser	Thr	Phe	Gln
			405						410					415	
Thr	Glu	Ala	Lys	Pro	Gly	Glu	Ala	Lys	Pro	Gln	Pro	Leu	Ser	Pro	Glu
		420						425				430			
Ser	Pro	Gln	Thr	Gly	Ser	Glu	Thr	Lys	Pro	Ala	Gly	Ser	Thr	Pro	Glu
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cctggagagg	ctaagcccca	gcccttgagt	cctgagtcac	cacagactgg	ctcagagacc	1320
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<211> 456

<212> PRT

<213> Rat

<400> 8

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			20						25					30	
Leu	Thr	Leu	Val	Tyr	Leu	Ile	Val	Phe	Val	Val	Gly	Ile	Leu	Gly	Asn
			35						40					45	
Ser	Val	Thr	Ile	Arg	Val	Thr	Gln	Val	Leu	Gln	Lys	Lys	Gly	Tyr	Leu
			50						55					60	
Gln	Lys	Glu	Val	Thr	Asp	His	Met	Ile	Ser	Leu	Ala	Cys	Ser	Asp	Ile
			65						70					75	
Leu	Val	Phe	Leu	Ile	Gly	Met	Pro	Met	Glu	Phe	Tyr	Ser	Ile	Ile	Trp
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Asn	Pro	Leu	Thr	Pro	Ser	Tyr	Ala	Leu	Ser	Cys	Lys	Leu	His	Thr	
			100						105					110	
Phe	Leu	Phe	Glu	Thr	Cys	Ser	Tyr	Ala	Thr	Leu	Leu	His	Val	Leu	Thr
			115						120					125	
Leu	Ser	Phe	Glu	Arg	Tyr	Ile	Ala	Ile	Cys	His	Pro	Phe	Arg	Tyr	Lys
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Asp	Val	Ser	Gly	Pro	Cys	Gln	Val	Lys	Leu	Leu	Ile	Gly	Phe	Val	Trp
			145						150					155	
Val	Thr	Ser	Ala	Leu	Val	Ala	Leu	Pro	Leu	Leu	Phe	Ala	Met	Gly	Ile
			165						170					175	
Glu	Tyr	Pro	Leu	Ala	Asn	Val	Pro	Thr	His	Lys	Gly	Leu	Asn	Cys	Asn
			180						185					190	
Leu	Ser	Arg	Thr	Arg	His	His	Asp	His	Pro	Gly	Asp	Ser	Asn	Met	Ser
			195						200					205	
Ile	Cys	Thr	Asn	Leu	Ser	Ser	Arg	Trp	Glu	Val	Phe	Gln	Ser	Ser	Ile
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Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile						
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Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile						
	290		295		300	
Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Lys Ser Tyr Phe Lys						
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Ala Tyr Met Ile Leu Leu Pro Phe Ser Asp Thr Phe Phe Tyr Leu Ser						
	325		330		335	
Ser Val Val Asn Pro Leu Leu Tyr Asn Val Ser Ser Gln Gln Phe Arg						
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Lys Val Phe Trp Gln Val Leu Cys Cys Arg Leu Thr Leu Gln His Ala						
	355		360		365	
Asn Gln Glu Lys Gln Gln Arg Ala Tyr Phe Ser Ser Thr Lys Asn Ser						
370	375		380			
Ser Arg Ser Ala Arg Ser Pro Leu Ile Phe Leu Ala Ser Arg Arg Ser						
385	390		395		400	
Asn Ser Ser Ser Arg Arg Thr Asn Lys Val Phe Leu Ser Thr Phe Gln						
	405		410		415	
Ala Glu Ala Lys Pro Leu Glu Gly Glu His Gln Pro Leu Ser Pro Glu						
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